

## SEQUENCE LISTING

## (1) GENERAL INFORMATION:

(i) APPLICANT: Ni, Jian  
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(ii) TITLE OF INVENTION: Death Domain Containing Receptor 5

(iii) NUMBER OF SEQUENCES: 12

(iv) CORRESPONDENCE ADDRESS:

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(E) COUNTRY: US  
(F) ZIP: 20850

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk  
(B) COMPUTER: IBM PC compatible  
(C) OPERATING SYSTEM: PC-DOS/MS-DOS  
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: US herewith  
(B) FILING DATE:  
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 60/054,021  
(B) FILING DATE: 29-JUL-1997

(viii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 60/040,846  
(B) FILING DATE: 17-MAR-1997

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## (2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1600 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 130..283

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 130..1362

(ix) FEATURE:

- (A) NAME/KEY: mat\_peptide
- (B) LOCATION: 284..1362

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CACCGCGTCCG CGGGCGCGGC CGGAGAACCC CGCAATCTTT GCGCCCACAA AATACACCGA	60
CGATGCCCGA TCTACTTTAA GGGCTGAAAC CCACGGGCCT GAGAGACTAT AAGAGCGTTC	120
CCTACCGCC ATG GAA CAA CGG GGA CAG AAC GCC CCG GCC GCT TCG GGG Met Glu Gln Arg Gly Gln Asn Ala Pro Ala Ala Ser Gly -51 -50 -45 -40	168
GCC CGG AAA AGG CAC GGC CCA GGA CCC AGG GAG GCG CGG GGA GCC AGG Ala Arg Lys Arg His Gly Pro Gly Pro Arg Glu Ala Arg Gly Ala Arg -35 -30 -25	216
CCT GGG CCC CGG GTC CCC AAG ACC CTT GTG CTC GTT GTC GCC GCG GTC Pro Gly Pro Arg Val Pro Lys Thr Leu Val Leu Val Val Ala Ala Val -20 -15 -10	264
CTG CTG TTG GTC TCA GCT GAG TCT GCT CTG ATC ACC CAA CAA GAC CTA Leu Leu Leu Val Ser Ala Glu Ser Ala Leu Ile Thr Gln Gln Asp Leu -5 1 5 10	312
GCT CCC CAG CAG AGA GCG GCC CCA CAA AAG AGG TCC AGC CCC TCA Ala Pro Gln Gln Arg Ala Ala Pro Gln Gln Lys Arg Ser Ser Pro Ser 15 20 25	360
GAG GGA TTG TGT CCA CCT GGA CAC CAT ATC TCA GAA GAC GGT AGA GAT Glu Gly Leu Cys Pro Pro Gly His His Ile Ser Glu Asp Gly Arg Asp 30 35 40	408
TGC ATC TCC TGC AAA TAT GGA CAG GAC TAT AGC ACT CAC TGG <u>AAT</u> GAC Cys Ile Ser Cys Lys Tyr Gly Gln Asp Tyr Ser Thr His Trp Asn Asp 45 50 55	456

CTC CTT TTC TGC TTG CGC TGC ACC AGG TGT GAT TCA GGT GAA GTG GAG Leu Leu Phe Cys Leu Arg Cys Thr Arg Cys Asp Ser Gly Glu Val Glu	60	65	70	504
CTA AGT CCC TGC ACC ACG ACC AGA AAC ACA GTG TGT CAG TGC GAA GAA Leu Ser Pro Cys Thr Thr Arg Asn Thr Val Cys Gln Cys Glu Glu	75	80	85	552
GGC ACC TTC CGG GAA GAA GAT TCT CCT GAG ATG TGC CGG AAG TGC CGC Gly Thr Phe Arg Glu Glu Asp Ser Pro Glu Met Cys Arg Lys Cys Arg	95	100	105	600
ACA GGG TGT CCC AGA GGG ATG GTC AAG GTC GGT GAT TGT ACA CCC TGG Thr Gly Cys Pro Arg Gly Met Val Lys Val Gly Asp Cys Thr Pro Trp	110	115	120	648
AGT GAC ATC GAA TGT GTC CAC AAA GAA TCA GGC ATC ATC ATA GGA GTC Ser Asp Ile Glu Cys Val His Lys Glu Ser Gly Ile Ile Ile Gly Val	125	130	135	696
ACA GTT GCA GCC GTA GTC TTG ATT GTG GCT GTG TTT GTT TGC AAG TCT Thr Val Ala Ala Val Val Leu Ile Val Ala Val Phe Val Cys Lys Ser	140	145	150	744
TTA CTG TGG AAG AAA GTC CTT CCT TAC CTG AAA GGC ATC TGC TCA GGT Leu Leu Trp Lys Lys Val Leu Pro Tyr Leu Lys Gly Ile Cys Ser Gly	155	160	165	792
GGT GGT GGG GAC CCT GAG CGT GTG-GAC <u>AGA</u> AGC TCA CAA CGA CCT GGG Gly Gly Asp Pro Glu Arg Val Asp Arg Ser Ser Gln Arg Pro Gly	175	180	185	840
GCT GAG GAC AAT GTC CTC AAT GAG ATC GTG AGT ATC TTG CAG CCC ACC Ala Glu Asp Asn Val Leu Asn Glu Ile Val Ser Ile Leu Gln Pro Thr	190	195	200	888
CAG GTC CCT GAG CAG GAA ATG GAA GTC CAG GAG CCA GCA GAG CCA ACA Gln Val Pro Glu Gln Glu Met Glu Val Gln Glu Pro Ala Glu Pro Thr	205	210	215	936
GGT GTC AAC ATG TTG TCC CCC GGG GAG TCA GAG CAT CTG CTG GAA CCG Gly Val Asn Met Leu Ser Pro Gly Glu Ser Glu His Leu Leu Glu Pro	220	225	230	984
GCA GAA GCT GAA AGG TCT CAG AGG AGG CTG CTG GTT CCA GCA AAT Ala Glu Ala Glu Arg Ser Gln Arg Arg Arg Leu Leu Val Pro Ala Asn	235	240	245	1032
GAA GGT GAT CCC ACT GAG ACT CTG AGA CAG TGC TTC GAT GAC TTT GCA Glu Gly Asp Pro Thr Glu Thr Leu Arg Gln Cys Phe Asp Asp Phe Ala	255	260	265	1080
GAC TTG GTG CCC TTT GAC TCC TGG GAG CCG CTC ATG AGG AAG TTG GGC Asp Leu Val Pro Phe Asp Ser Trp Glu Pro Leu Met Arg Lys Leu Gly	270	275	280	1128

CTC ATG GAC AAT GAG ATA AAG GTG GCT AAA GCT GAG GCA GCG GGC CAC Leu Met Asp Asn Glu Ile Lys Val Ala Lys Ala Glu Ala Ala Gly His 285 290 295	1176
AGG GAC ACC TTG TAC ACG ATG CTG ATA AAG TGG GTC AAC AAA ACC GGG Arg Asp Thr Leu Tyr Thr Met Leu Ile Lys Trp Val Asn Lys Thr Gly 300 305 310	1224
CGA GAT GCC TCT GTC CAC ACC CTG CTG GAT GCC TTG GAG ACG CTG GGA Arg Asp Ala Ser Val His Thr Leu Leu Asp Ala Leu Glu Thr Leu Gly 315 320 325 330	1272
GAG AGA CTT GCC AAG CAG AAG ATT GAG GAC CAC TTG TTG AGC TCT GGA Glu Arg Leu Ala Lys Gln Lys Ile Glu Asp His Leu Leu Ser Ser Gly 335 340 345	1320
AAG TTC ATG TAT CTA GAA GGT AAT GCA GAC TCT GCC ATG TCC Lys Phe Met Tyr Leu Glu Gly Asn Ala Asp Ser Ala Met Ser 350 355 360	1362
TAAGTGTGAT TCTCTTCAGG AAGTGAGACC TTCCCTGGTT TACCTTTTTT CTGGAAAAAG	1422
CCCAACTGGA CTCCAGTCAG TAGGAAAGTG CCACAATTGT CACATGACCG GTACTGGAAG	1482
AAACTCTCCC ATCCAACATC ACCCAGTGGGA TGGAACATCC TGTAACCTTT CACTGCACTT	1542
GGCATTATTT TTATAAGCTG AATGTGATAA TAAGGACACT ATGGAAAAAA AAAAAAAA	1600

## (2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 411 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Glu Gln Arg Gly Gln Asn Ala Pro Ala Ala Ser Gly Ala Arg Lys  
-51 -50 -45 -40

Arg His Gly Pro Gly Pro Arg Glu Ala Arg Gly Ala Arg Pro Gly Pro  
-35 -30 -25 -20

Arg Val Pro Lys Thr Leu Val Leu Val Ala Ala Val Leu Leu Leu  
-15 -10 -5

Val Ser Ala Glu Ser Ala Leu Ile Thr Gln Gln Asp Leu Ala Pro Gln  
1 5 10

Gln Arg Ala Ala Pro Gln Gln Lys Arg Ser Ser Pro Ser Glu Gly Leu  
15 20 25

Cys Pro Pro Gly His His Ile Ser Glu Asp Gly Arg Asp Cys Ile Ser  
 30 35 40 45  
 Cys Lys Tyr Gly Gln Asp Tyr Ser Thr His Trp Asn Asp Leu Leu Phe  
 50 55 60  
 Cys Leu Arg Cys Thr Arg Cys Asp Ser Gly Glu Val Glu Leu Ser Pro  
 65 70 75  
 Cys Thr Thr Thr Arg Asn Thr Val Cys Gln Cys Glu Glu Gly Thr Phe  
 80 85 90  
 Arg Glu Glu Asp Ser Pro Glu Met Cys Arg Lys Cys Arg Thr Gly Cys  
 95 100 105  
 Pro Arg Gly Met Val Lys Val Gly Asp Cys Thr Pro Trp Ser Asp Ile  
 110 115 120 125  
 Glu Cys Val His Lys Glu Ser Gly Ile Ile Ile Gly Val Thr Val Ala  
 130 135 140  
 Ala Val Val Leu Ile Val Ala Val Phe Val Cys Lys Ser Leu Leu Trp  
 145 150 155  
 Lys Lys Val Leu Pro Tyr Leu Lys Gly Ile Cys Ser Gly Gly Gly  
 160 165 170  
 Asp Pro Glu Arg Val Asp Arg Ser Ser Gln Arg Pro Gly Ala Glu Asp  
 175 180 185  
 Asn Val Leu Asn Glu Ile Val Ser Ile Leu Gln Pro Thr Gln Val Pro  
 190 195 200 205  
 Glu Gln Glu Met Glu Val Gln Glu Pro Ala Glu Pro Thr Gly Val Asn  
 210 215 220  
 Met Leu Ser Pro Gly Glu Ser Glu His Leu Leu Glu Pro Ala Glu Ala  
 225 230 235  
 Glu Arg Ser Gln Arg Arg Arg Leu Leu Val Pro Ala Asn Glu Gly Asp  
 240 245 250  
 Pro Thr Glu Thr Leu Arg Gln Cys Phe Asp Asp Phe Ala Asp Leu Val  
 255 260 265  
 Pro Phe Asp Ser Trp Glu Pro Leu Met Arg Lys Leu Gly Leu Met Asp  
 270 275 280 285  
 Asn Glu Ile Lys Val Ala Lys Ala Glu Ala Ala Gly His Arg Asp Thr  
 290 295 300  
 Leu Tyr Thr Met Leu Ile Lys Trp Val Asn Lys Thr Gly Arg Asp Ala  
 305 310 315

Ser Val His Thr Leu Leu Asp Ala Leu Glu Thr Leu Gly Glu Arg Leu  
 320 325 330

Ala Lys Gln Lys Ile Glu Asp His Leu Leu Ser Ser Gly Lys Phe Met  
 335 340 345

Tyr Leu Glu Gly Asn Ala Asp Ser Ala Met Ser  
 350 355 360

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 455 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Met Gly Leu Ser Thr Val Pro Asp Leu Leu Leu Pro Leu Val Leu Leu  
 1 5 10 15

Glu Leu Leu Val Gly Ile Tyr Pro Ser Gly Val Ile Gly Leu Val Pro  
 20 25 30

His Leu Gly Asp Arg Glu Lys Arg Asp Ser Val Cys Pro Gln Gly Lys  
 35 40 45

Tyr Ile His Pro Gln Asn Asn Ser Ile Cys Cys Thr Lys Cys His Lys  
 50 55 60

Gly Thr Tyr Leu Tyr Asn Asp Cys Pro Gly Pro Gln Asp Thr Asp  
 65 70 75 80

Cys Arg Glu Cys Glu Ser Gly Ser Phe Thr Ala Ser Glu Asn His Leu  
 85 90 95

Arg His Cys Leu Ser Cys Ser Lys Cys Arg Lys Glu Met Gly Gln Val  
 100 105 110

Glu Ile Ser Ser Cys Thr Val Asp Arg Asp Thr Val Cys Gly Cys Arg  
 115 120 125

Lys Asn Gln Tyr Arg His Tyr Trp Ser Glu Asn Leu Phe Gln Cys Phe  
 130 135 140

Asn Cys Ser Leu Cys Leu Asn Gly Thr Val His Leu Ser Cys Gln Glu  
 145 150 155 160

Lys Gln Asn Thr Val Cys Thr Cys His Ala Gly Phe Phe Leu Arg Glu

	165	170	175
Asn Glu Cys Val Ser Cys Ser Asn Cys Lys Lys Ser Leu Glu Cys Thr			
180	185	190	
Lys Leu Cys Leu Pro Gln Ile Glu Asn Val Lys Gly Thr Glu Asp Ser			
195	200	205	
Gly Thr Thr Val Leu Leu Pro Leu Val Ile Phe Phe Gly Leu Cys Leu			
210	215	220	
Leu Ser Leu Leu Phe Ile Gly Leu Met Tyr Arg Tyr Gln Arg Trp Lys			
225	230	235	240
Ser Lys Leu Tyr Ser Ile Val Cys Gly Lys Ser Thr Pro Glu Lys Glu			
245	250	255	
Gly Glu Leu Glu Gly Thr Thr Lys Pro Leu Ala Pro Asn Pro Ser			
260	265	270	
Phe Ser Pro Thr Pro Gly Phe Thr Pro Thr Leu Gly Phe Ser Pro Val			
275	280	285	
Pro Ser Ser Thr Phe Thr Ser Ser Thr Tyr Thr Pro Gly Asp Cys			
290	295	300	
Pro Asn Phe Ala Ala Pro Arg Arg Glu Val Ala Pro Pro Tyr Gln Gly			
305	310	315	320
Ala Asp Pro Ile Leu Ala Thr Ala Leu Ala Ser Asp Pro Ile Pro Asn			
325	330	335	
Pro Leu Gln Lys Trp Glu Asp Ser Ala His Lys Pro Gln Ser Leu Asp			
340	345	350	
Thr Asp Asp Pro Ala Thr Leu Tyr Ala Val Val Glu Asn Val Pro Pro			
355	360	365	
Leu Arg Trp Lys Glu Phe Val Arg Arg Leu Gly Leu Ser Asp His Glu			
370	375	380	
Ile Asp Arg Leu Glu Leu Gln Asn Gly Arg Cys Leu Arg Glu Ala Gln			
385	390	395	400
Tyr Ser Met Leu Ala Thr Trp Arg Arg Arg Thr Pro Arg Arg Glu Ala			
405	410	415	
Thr Leu Glu Leu Leu Gly Arg Val Leu Arg Asp Met Asp Leu Leu Gly			
420	425	430	
Cys Leu Glu Asp Ile Glu Glu Ala Leu Cys Gly Pro Ala Ala Leu Pro			
435	440	445	
Pro Ala Pro Ser Leu Leu Arg			
450	455		

## (2) INFORMATION FOR SEQ ID NO:4:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 335 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met	Leu	Gly	Ile	Trp	Thr	Leu	Leu	Pro	Leu	Val	Leu	Thr	Ser	Val	Ala
1						5					10	-			15
Arg Leu Ser Ser Lys Ser Val Asn Ala Gln Val Thr Asp Ile Asn Ser															
						20				25				30	
Lys Gly Leu Glu Leu Arg Lys Thr Val Thr Val Glu Thr Gln Asn															
						35			40				45		
Leu Glu Gly Leu His His Asp Gly Gln Phe Cys His Lys Pro Cys Pro															
						50			55				60		
Pro Gly Glu Arg Lys Ala Arg Asp Cys Thr Val Asn Gly Asp Glu Pro															
						65			70				75		80
Asp Cys Val Pro Cys Gln Glu Gly Lys Glu Tyr Thr Asp Lys Ala His															
						85			90				95		
Phe Ser Ser Lys Cys Arg Arg Cys Arg Leu Cys Asp Glu Gly His Gly															
						100			105				110		
Leu Glu Val Glu Ile Asn Cys Thr Arg Thr Gln Asn Thr Lys Cys Arg															
						115			120				125		
Cys Lys Pro Asn Phe Phe Cys Asn Ser Thr Val Cys Glu His Cys Asp															
						130			135				140		
Pro Cys Thr Lys Cys Glu His Gly Ile Ile Lys Glu Cys Thr Leu Thr															
						145			150				155		160
Ser Asn Thr Lys Cys Lys Glu Glu Gly Ser Arg Ser Asn Leu Gly Trp															
						165			170				175		
Leu Cys Leu Leu Leu Pro Ile Pro Leu Ile Val Trp Val Lys Arg															
						180			185				190		
Lys Glu Val Gln Lys Thr Cys Arg Lys His Arg Lys Glu Asn Gln Gly															
						195			200				205		

Ser His Glu Ser Pro Thr Leu Asn Pro Glu Thr Val Ala Ile Asn Leu  
 210 215 220

Ser Asp Val Asp Leu Ser Lys Tyr Ile Thr Thr Ile Ala Gly Val Met  
 225 230 235 240

Thr Leu Ser Gln Val Lys Gly Phe Val Arg Lys Asn Gly Val Asn Glu  
 245 250 255

Ala Lys Ile Asp Glu Ile Lys Asn Asp Asn Val Gln Asp Thr Ala Glu  
 260 265 270

Gln Lys Val Gln Leu Leu Arg Asn Trp His Gln Leu His Gly Lys Lys  
 275 280 285

Glu Ala Tyr Asp Thr Leu Ile Lys Asp Leu Lys Lys Ala Asn Leu Cys  
 290 295 300

Thr Leu Ala Glu Lys Ile Gln Thr Ile Ile Leu Lys Asp Ile Thr Ser  
 305 310 315 320

Asp Ser Glu Asn Ser Asn Phe Arg Asn Glu Ile Gln Ser Leu Val  
 325 330 335

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 417 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Met Glu Gln Arg Pro Arg Gly Cys Ala Ala Val Ala Ala Ala Leu Leu  
 1 5 10 15

Leu Val Leu Leu Gly Ala Arg Ala Gln Gly Gly Thr Arg Ser Pro Arg  
 20 25 30

Cys Asp Cys Ala Gly Asp Phe His Lys Lys Ile Gly Leu Phe Cys Cys  
 35 40 45

Arg Gly Cys Pro Ala Gly His Tyr Leu Lys Ala Pro Cys Thr Glu Pro  
 50 55 60

Cys Gly Asn Ser Thr Cys Leu Val Cys Pro Gln Asp Thr Phe Leu Ala  
 65 70 75 80

Trp Glu Asn His His Asn Ser Glu Cys Ala Arg Cys Gln Ala Cys Asp

85

90

95

Glu Gln Ala Ser Gln Val Ala Leu Glu Asn Cys Ser Ala Val Ala Asp  
 100 105 110

Thr Arg Cys Gly Cys Lys Pro Gly Trp Phe Val Glu Cys Gln Val Ser  
 115 120 125

Gln Cys Val Ser Ser Ser Pro Phe Tyr Cys Gln Pro Cys Leu Asp Cys  
 130 135 140

Gly Ala Leu His Arg His Thr Arg Leu Leu Cys Ser Arg Arg Asp Thr  
 145 150 155 160

Asp Cys Gly Thr Cys Leu Pro Gly Phe Tyr Glu His Gly Asp Gly Cys  
 165 170 175

Val Ser Cys Pro Thr Ser Thr Leu Gly Ser Cys Pro Glu Arg Cys Ala  
 180 185 190

Ala Val Cys Gly Trp Arg Gln Met Phe Trp Val Gln Val Leu Leu Ala  
 195 200 205

Gly Leu Val Val Pro Leu Leu Leu Gly Ala Thr Leu Thr Tyr Thr Tyr  
 210 215 220

Arg His Cys Trp Pro His Lys Pro Leu Val Thr Ala Asp Glu Ala Gly  
 225 230 235 240

Met Glu Ala Leu Thr Pro Pro Pro Ala Thr His Leu Ser Pro Leu Asp  
 245 250 255

Ser Ala His Thr Leu Leu Ala Pro Pro Asp Ser Ser Glu Lys Ile Cys  
 260 265 270

Thr Val Gln Leu Val Gly Asn Ser Trp Thr Pro Gly Tyr Pro Glu Thr  
 275 280 285

Gln Glu Ala Leu Cys Pro Gln Val Thr Trp Ser Trp Asp Gln Leu Pro  
 290 295 300

Ser Arg Ala Leu Gly Pro Ala Ala Ala Pro Thr Leu Ser Pro Glu Ser  
 305 310 315 320

Pro Ala Gly Ser Pro Ala Met Met Leu Gln Pro Gly Pro Gln Leu Tyr  
 325 330 335

Asp Val Met Asp Ala Val Pro Ala Arg Arg Trp Lys Glu Phe Val Arg  
 340 345 350

Thr Leu Gly Leu Arg Glu Ala Glu Ile Glu Ala Val Glu Val Glu Ile  
 355 360 365

Gly Arg Phe Arg Asp Gln Gln Tyr Glu Met Leu Lys Arg Trp Arg Gln  
 370 375 380

Gln Gln Pro Ala Gly Leu Gly Ala Val Tyr Ala Ala Leu Glu Arg Met  
 385 390 395 400

Gly Leu Asp Gly Cys Val Glu Asp Leu Arg Ser Arg Leu Gln Arg Gly  
 405 410 415

Pro

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 507 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

AATTCGGCAC AGCTCTTCAG	GAAGTCAGAC	CTTCCCTGGT	TTACCTTTT	TCTGGAAAAA	60	
GCCCAACTGG	GACTCCAGTC	AGTAGGAAAG	TGCCACAATT	GTCACATGAC	CGGTACTGGA	120
AGAAACTCTC	CCATCCAACA	TCACCCAGTG	GNATGGAAC	ACTGATGAAC	TTTCACTGC	180
ACTTGGCATT	ATTTTGTNA	AGCTGAATGT	GATAATAAGG	GCACTGATGG	AAATGTCTGG	240
ATCATTCCGG	TTGTGCGTAC	TTTGAGATT	GNNGTTGGGG	ATGTNCATTG	TGTTTGACAG	300
CACTTTTTN	ATCCCTAACATG	TNAAATGCNT	NATTTGATTG	TGANTTGGGG	GTNAACATTG	360
GTNAAGGNTN	CCCNTNTGAC	ACAGTAGNTG	GTNCCCGACT	TANAATNGNN	GAANANGATG	420
NATNANGAAC	CTTTTTTGG	GTGGGGGGGT	NNCGGGCAG	TNNAANGNNG	NCTCCCCAGG	480
TTTGGNGTNG	CAATNGNGGA	ANNNTGG				507

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 226 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

TTTTTTTGATAGATGGATCT TACAATGTAG CCCAAATAAA TAAATAAAGC ATTTACATTA	60
GGATAAAAAA GTGCTGTGAA ACAATGACA TCCCAAACCA AATCTCAAAG TACGCACAAA	120
CGGAATGATC CAGACATTTC CATAGGTCCCT TATTATCACA TTCAGCTTAT AAAATAATGC	180
CAAGTGCAGT GAAAAGTTAC AGGATGTTCC ATCCACTGGG TGGATT	226

## (2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 25 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA (genomic)

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

CGCCCATGGA GTCTGCTCTG ATCAC	25
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## (2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 30 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA (genomic)

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

CGCAAGCTTT TAGCCTGATT CTTTGTGGAC	30
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## (2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 36 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

CGCGGATCCG CCATCATGG ACAAACGGGG A CAGAAC

36

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

CGCGGTACCT TAGGACATGG CAGAGTC

27

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

CGCGGTACCT TAGCCTGATT CTTTGTGGAC

30